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EXAMINER	
NEGIN, RUSSELL SCOTT	
ART UNIT	PAPER NUMBER
1631	

NOTIFICATION DATE	DELIVERY MODE
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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

IPOPS.LEGAL@agilent.com

Office Action Summary	Application No.	Applicant(s)	
	10/817,244	YAKHINI ET AL.	
	Examiner	Art Unit	
	RUSSELL S. NEGIN	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07 January 2008*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-56 and 80-100* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-56,80-90 and 92-94* is/are rejected.

7)☒ Claim(s) *91 and 95-100* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Comments

Applicants' amendments and request for reconsideration in the communication filed on 7 January 2008 are acknowledged and the amendments are entered.

Claims 1-56 and 80-100 are pending and examined in the instant Office action.

Withdrawn Rejections

The rejections of claims 1-56 under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement are withdrawn in view of amendments to the instant set of claims filed on 7 January 2008.

The rejections of claims 1-3, 7, 12-15, and 27-28 under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. [Genome Research, 2000, volume 10, pages 365-378] are withdrawn in view of amendments to the instant set of claims filed on 7 January 2008.

The rejections of claims 16, 18, 20-26, 29-33, and 55-56 under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in further view of Stanyon et al. [Cytogenetics and Cell Genetics, volume 84, 1999, pages 150-155] are withdrawn in view of amendments to the instant set of claims filed on 7 January 2008.

The rejections of claims 17 and 19 under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Stanyon et al. in view of Singer et al. [US Patent

5,866,331] are withdrawn in view of amendments to the instant set of claims filed on 7 January 2008.

Claim Objections

Claims 91 and 95-100 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Claims 91 and 95-100 recite the use of four microarrays with different specific statistical properties.

These features of the above claims are not taught or made obvious in the prior art.

Claim Rejections - 35 USC § 112

The following rejection is newly applied:

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claim 88 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

In this claim it is unclear what is meant by a distance between locations and scores. A location has physical units (i.e. meters), while a score has dimensionless

units. Since a location has physically distinct units that a score, it is unclear what is meant by this distance and the units that it possesses (i.e. physical or dimensionless).

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

The following 35 U.S.C. 103 Rejections are newly applied:

35 U.S.C. 103 Rejection #1:

Claims 1-15 and 27-28 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. [Genome Research, 2000, volume 10, pages 365-378]

in view of Koleszar et al. [US Patent 6,519,583; issued 11 February 2003; filed 27 July 1999].

Claim 1 is drawn to a method for overlaying gene- or protein-related data on chromosome maps, said method comprising the steps of:

--importing arbitrary gene- or protein-related data and having identifiers for determining genetic loci of genes to which said arbitrary gene-related data are associated;

--matching the identifiers with predefined identifiers on at least one of the chromosome maps; and

--displaying the arbitrary gene- or protein related data adjacent positions on the at least one chromosome map where the genes associated with the respective arbitrary gene or protein-related data are located according to said matching the identifiers with the predefined identifiers, wherein said importing, reading, matching and displaying are all automated steps.

Claim 4-6 and 8-11 are dependent from claim 1 with the additional features of displaying the genetic data is a specific means wherein each claim identifies a separate feature used to display the data.

The article of Ben-Dor et al., entitled, "RHO-Radiation Hybrid Ordering" states in its abstract:

> Radiation hybrid (RH) mapping is a somatic cell technique that is used for ordering markers along a chromosome and estimating the physical distances between them. With the advent of this mapping technique, analyzing the experimental data is becoming a challenging and demanding computational task. In this paper we present the software package RHO (radiation hybrid ordering). This package implements a number of heuristics to order genomic markers along a chromosome, given as input the results of an RH experiment.

The gene data is imported from the Whitehead Institute (the external source) as stated in the lines bridging columns 1 and 2 of page 368 of Ben-Dor et al.:

> The RH data used to construct the maps was downloaded from the Whitehead Institute for Biomedical Research.

Identifiers are listed in Table 4 of page 371 of Ben-Dor et al. and the matching process is described in lines 7-23 of column 2 of page 371 to lines 1-5 of column 1 of page 372:

> Different maps of the same chromosome give rise to different estimates of its total physical length. Shorter maps are generally viewed as more desirable ones. This transformation of probabilities to distances is implemented in RHMAPPER. Using this implementation, we conclude that the total physical length of chromosome 2 in our map is 3.88% shorter that in the WI framework map... The detailed differences between the two maps are depicted graphically in Figure 6. These map portions are drawn to scale.

Consequently, Figure 6 of Ben-Dor et al. maps the chromosome identifiers between the chromosome 2 map and the WI framework map. The data in Figure 6 of Ben-Dor et al. are spatially grouped on the chromosome map. There is a plurality of chromosome maps illustrated in Figure 6 of Ben-Dor et al.

Page 370 of Ben-Dor et al. devotes this technique for "A New Map of Chromosome 2," indicating that the relevant data has not already been mapped to a chromosome (i.e. it is a new chromosome map).

Ben-Dor et al. does not explicitly state that every step corresponding to the instant claim is automated and Ben-Dor et al. does not teach the required display techniques.

The invention of Koleszar et al., entitled, "Graphical viewer for biomolecular sequence data," states in the abstract:

> Disclosed are methods, media and systems for graphically displaying computer-based biomolecular sequence information. Generally, biomolecular sequence information may be

> graphically depicted in a variety of different forms in accordance with the present invention. The sequence information may be composed of nucleotide or amino acid sequence information or both. The graphical depictions may be in several different formats providing different information relating to the sequences, and may be displayed in one or more screens of a computer user interface.

Figure 4A has the ability to zoom in on regions or zooming out and compressing regions of the genomic sequence of interest as is illustrated on the toolbar of the schematic with pop-up buttons to control the viewing of the features.

The purpose of Koleszar et al. in explained in column 2, lines 5-9, which states:

> Accordingly, the development if a display tool which allows a user to clearly and effectively display gene loci information for a given organism or organisms and/or other biomolecular sequences in desirable.

Consequently, Koleszar et al. describes a user friendly, convenient, and effective display of gene loci information.

Claim 2 is further limiting with the additional limitation of further comprising interactive selection by a user of at least one data type to be displayed during said displaying.

Figure 6 of Ben-Dor et al. schematically diagrams the data types of the sequence identifiers.

Claim 3 is further limiting with the additional limitation of further comprising spatially grouping said gene- or protein related data to correspond to spatial groupings of said associated genes on said at least one chromosome map.

Figure 6 of Ben-Dor et al. illustrates spatial groupings of chromosome maps and relations with WI framework maps.

Claim 7 is further limiting with the additional limitation of maintaining focus and context of at least a portion of the display of said chromosome maps and gene or protein-related data.

Figure 6 of Ben-Dor et al. illustrates a plurality of chromosome maps with focuses on portions of each chromosome map.

Claim 12 is further limiting with the additional limitation of further comprising accessing an external source of information relative to the data displayed, matching at least one of said identifiers with specific information in said external source, and displaying said specific information relative to said gene or protein-related data associated with said at least one identifier.

Figure 6 of Ben-Dor et al. illustrates matching data of chromosome maps with external sources, and displaying said information with an identifier.

Claim 13 is further limiting with the additional limitation that the identifiers of said arbitrary gene or protein related data are selected from published gene identifiers and symbols.

Claim 14 is further limiting with such a given list of symbol types.

The identifier symbols in Figure 6 of Ben-Dor et al. correspond to such required identifiers.

Claim is further limiting with the additional limitation that the matching comprises providing a relational database which stores a set of cross-referenced tables for matching said identifiers with said predefined identifiers.

Figure 6 of Ben-Dor et al. illustrates a relational database between chromosome maps and a WI framework map with the proper predefined identifiers.

Claim 27 is further limiting with the additional limitation that said arbitrary gene or protein data is imported from a plurality of experiments.

Claim 28 is further limiting with the additional limitation that said gene or protein data is displayed with regard to each of the plurality of experiments on a single display.

Figure 6 of Ben-Dor et al. illustrates such a plurality of graphs based on a plurality of experiments.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the chromosome mapping technique of Ben-Dor et al. by use of the automated gene display method of Koleszar et al., wherein the motivation would have been that Koleszar et al. has the advantage of displaying the genomic data of Ben-Dor et al. in a more convenient and user-friendly format [see, for example, column 2, lines 5-9 of Koleszar et al.].

Response to Arguments:

Applicant's arguments filed 7 January 2008 have been fully considered but they are not persuasive.

Applicant first argues that Ben-Dor et al. does not teach arbitrary gene or protein related data. This is not found to be persuasive because given the broad nature of this term, Ben-Dor et al. teaches arbitrary genetic and protein related data because this broad term encompass the genetic markers listed in Table 4 of Ben-Dor et al., which are related to genes.

Applicant also argues that Ben-Dor et al. does not teach reading of identifiers associated with gene or protein related data. This is not found persuasive because given the broad meaning of identifiers, Figure 6 incorporate and map identifiers to predefined identifiers.

Applicant also argues that the amended claims recite the limitation that arbitrary gene or protein related data are displayed at adjacent positions in the chromosome map. This is not found to be persuasive, because the predefined identifiers (i.e. Whitehead) are displayed adjacent to the identifiers of Ben-Dor et al in Figure 6 of Ben-Dor et al.

With regards to Koleszar et al., applicant argues that Koleszar et al. does not teach the alleged missing limitations of Ben-Dor et al. Since the Ben-Dor et al. is not deficient, the reference of Ben-Dor et al, when combined with the invention of Koleszar et al. teaches all of the limitations in the instant set of claims.

The following 35 U.S.C. 103 Rejections are newly applied:

35 U.S.C. 103 Rejection #2:

Claims 16, 18, 20-26, 29-33, and 55-56 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Koleszar et al. as applied to claims 1-15, and 27-28 above in further view of Stanyon et al. [Cytogenetics and Cell Genetics, volume 84, 1999, pages 150-155].

Claim 16 is further limiting with the additional limitation that the gene related data comprises a expression matrix.

Claim 18 is further limiting with the additional limitation that said arbitrary gene or protein-related data comprises a matrix of at least one microarray of gene data wherein each row of the matrix is associated with a particular gene and wherein said matching comprises reordering and spatial grouping of the rows based on matching the identifiers to the predefined identifiers.

Ben-Dor et al. and Koleszar et al. make obvious an automated method for mapping genetic information, as discussed above.

Ben-Dor et al. and Koleszar et al. do not teach the claimed matrix limitations of the instant claims.

The article of Stanyon et al., entitled, "Reciprocal chromosome painting shows that genomic rearrangement between rat and mouse proceeds ten times faster than between humans and cats," states in the first sentence of the abstract:

> Reciprocal chromosome painting between mouse and rat using complete chromosome probe sets of both species permitted us to assign chromosomal homology between these rodents.

The purpose of the study is explained on page 151, column 1, lines 7-10, which state:

> Reciprocal chromosome painting between rat and mouse allows a transfer of gene mapping data from mouse to rat and vice versa, thus aiding in both disease and genetic trait analyses.

The annotated chromosome maps of the rat and mouse are shown in Figures 3 and 4 of page 152 of Stanyon et al. The numbers annotations are used for the comparison of rat to mouse genetic homologies.

A matrix is shown which compares the expression data between mouse and rat on page 153 of Stanyon et al. in which similarities are scored by coloring the tiles in the matrices.

Claim 20 is further limiting with the additional limitation of further comprising statistically assessing co-location values and displaying assessed co-location statistical significance along side said arbitrary gene-related data.

Claim 21 is further limiting with the additional limitation of displaying said genetic information of the chromosome map of the respective genes.

The statistics of each row and column of the matrix are enumerated in numbers that border each row and column of the matrix in Figure 5 of Stanyon et al. These statistics represent the percent agreement between FISH and gene mapping. The matrix is color coded according the expression data and the clusters of data are evaluated in the numbers bordering each column and row on the matrix.

Claim 22 is further limiting with the additional limitation of having the data comprise annotations.

Claim 23 is further limiting with the additional limitation that the annotations are related to gene otology.

Claim 24 is further limiting with the additional limitation that the additional information is taken from relevance scores.

Claim 25 is further limiting with the additional limitation that the additional limitation is displayed in matrix form.

Claim 26 is further limiting wherein the arbitrary gene and protein data is displayed in a scatter plot format.

The statistics of each row and column of the matrix are enumerated in numbers that border each row and column of the matrix in Figure 5 of Stanyon et al. The squares in this scatter plot or matrix have numbers on them to indicate relevance with FISH. These statistics represent the percent agreement between FISH and gene mapping. The matrix is color coded according the expression data and the clusters of data are evaluated in the numbers bordering each column and row on the matrix.

Claim 29 is further limiting with the limitation that the additional data comprises statistical data.

Statistical data is displayed along side the matrix shown in Figure 5 of Stanyon et al.

Claim 30 is further limiting with the additional limitation that calculating values for each row and an auxiliary process for obtaining cluster data for said row vectors and displaying such data.

Claim 31 is further limiting with the additional limitation that the matrix comprises a heat map.

Claim 32 is further limiting with the additional limitation that the cluster data is displayed adjacent each matrix.

Claim 33 is further limiting with the additional limitation that the cluster data is displayed in multiple columns.

Figure 5 of Stanyon et al. illustrates a matrix of results around the checker-board "heat map" or matrix.

Claims 55 and 56 are further limiting with the additional limitation of selecting additional information related to one or more genes and displaying this information along the side of the matrix. Claim 56 lists the types of information that qualify as possible data.

Figure 5 of Stanyon et al. illustrates a matrix of annotations results around the checker-board "heat map" or matrix.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the radiation hybrid ordering method of Ben-Dor et al. the display method of Koleszar et al. by use of the homology study of Stanyon et al.

because while Ben-Dor et al. examines differences in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determine similarities between the genomes of different species to aid in disease and genetic trait analyses [see title and abstract of Stanyon et al.].

Response to Arguments:

Applicant's arguments filed 7 January 2008 have been fully considered but they are not persuasive.

First, applicant argues for the reasons above, that the Ben-Dor et al. reference is deficient. This is not found persuasive because, for the reasons discussed above, the examiner maintains that Ben-Dor et al. teaches the argued limitations and that the combination of references make obvious the claimed invention.

Applicant then argues that Stanyon et al. does not cure these alleged deficiencies of Ben-Dor et al. For the reasons discussed above, the examiner maintains that Ben-Dor et al. teaches the argued limitations.

Applicant next argues that there is no motivation to combine Ben-Dor et al. and Stanyon et al. This argument is not persuasive because, as recited above:

> Stanyon et al. uses these techniques of mapping and matching to determining similarities between the genomes of different species to aid in disease and genetic trait analyses.

Consequently, there would have been a reasonable expectation of success in combining the references because the study of Stanyon et al. is a direct application of Ben-Dor et al. as applied to determining sequence homology between different species.

The motivation, as recited above, states the following:

> It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the radiation hybrid ordering method of Ben-Dor et al. the display method of Koleszar et al. by use of the homology study of Stanyon et al. because while Ben-Dor et al. examines differences in databases and labeling techniques through chromosome mapping and matching, Stanyon et al. uses these techniques of mapping and matching to determine similarities between the genomes of different species to aid in disease and genetic trait analyses [see title and abstract of Stanyon et al.].

The following 35 U.S.C. 103 Rejections are newly applied:

35 U.S.C. 103 Rejection #3:

Claims 17 and 19 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Koleszar et al. in view of Stanyon et al. as applied to claims 1-16, 18, 20-28, 29-33, and 55-56 above in further view of Singer et al. [US Patent 5,866,331].

Claim 17 is further limiting with the additional limitation of having a plurality of matrices.

Claim 19 is further limiting with the additional limitation of comprising a heat map in the plurality of matrices.

Ben-Dor et al., Koleszar et al., and Stanyon et al. make obvious an automated method for mapping genetic information, as discussed above.

Ben-Dor et al., Koleszar et al., and Stanyon et al. fail to teach heat maps on a plurality of matrices.

The invention of Singer et al., entitled, "Single molecule detection by in situ hybridization," states that its purpose is to use cell microscopy, biology, and digital imaging to better detect shorter target sequences. As is stated in column 4, lines 49-51,

"As few as five fluorochromes on a single probe provide a sufficiently strong signal for a detection of that single probe."

Figures 2A and 2B illustrate a plurality of heat maps used to detect hybridizations to nucleotide probes.

It would have been obvious at the time of the instant invention for someone of ordinary skill in the art to modify the radiation hybridization ordering study of Ben-Dor et al., the display technique of Koleszar et al. and the homology determination method of Stanyon et al. by use of the heat maps shown in Singer et al. wherein the motivation would have been that Singer et al. uses advanced mapping techniques to better detect hybridization to short target sequences [see for example, Figure 2 of Singer et al.].

Response to Arguments:

Applicant's arguments filed 7 January 2008 have been fully considered and they are persuasive.

First, applicant argues for the reasons above, that the Ben-Dor et al. reference is deficient. This is not found persuasive because, for the reasons discussed above, the examiner maintains that Ben-Dor et al. teaches the argued limitations.

Applicant then argues that Singer et al. does not cure these alleged deficiencies of Ben-Dor et al. For the reasons discussed above, the examiner maintains that Ben-Dor et al. teaches the argued limitations, and that the combination of references make obvious the claimed invention.

The following 35 U.S.C. 103 Rejections are newly applied:

35 U.S.C. 103 Rejection #4:

Claim 80 is rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Koleszar et al. as applied to claims 1-15 and 27-28 above, and further in view of Bodzin et al. [US PGPUB 2003/0139886 A1 published 24 July 2003; filed 5 September 2002].

Independent claim 80 is drawn to the same subject matter as instant claim 1 with the additional limitation of dividing a microarray into a first control matrix and a second experimental matrix.

Ben-Dor et al. and Koleszar et al. make obvious an automated method for mapping and matching genetic information, as discussed above.

Ben-Dor et al. and Koleszar et al. fail to teach the division of the microarray of interest into an experimental and control matrix.

Bodzin et al. teaches a method and apparatus for normalization and deconvolution of assay data.

For example, Figure 15 of Bodzin et al. illustrates the division of a microarray.

Furthermore, paragraph [0575] describes uses of controls for normalization of the remaining data.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the radiation hybrid ordering method of Ben-Dor et al. and the display method of Koleszar et al. by use of the microarray division method of Bodzin et al. wherein the motivation would have been that the use of controls in

microarrays provide a convenient means of normalization of the instant set of data [see paragraph 0037 of Bodzin et al.]

The following 35 U.S.C. 103 Rejections are newly applied:

35 U.S.C. 103 Rejection #5:

Claims 81-83, 85-87, 90 and 93-94 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Koleszar et al. in view of Stanyon et al. as applied to claims 1-16, 18, 20-28, 29-33, and 55-56 above, and further in view of Bodzin et al.

Claim 81 is further limiting wherein the matrices are displayed as heat maps.

Claim 82 is further limiting wherein the matrices are compared.

Claim 83 is further limiting wherein the calculating occurs using a user interface.

Claim 85 is further limiting wherein the scores are displayed on a line map.

Claim 86 is further limiting wherein the relevance scores are displayed on a heat map.

Claim 87 is further limiting wherein the scores are calculated and displayed in a binary code.

Claim 90 is further limiting wherein matching chromosomal copy abnormality data with the gene related data identifiers and displaying this data along side the gene-related data.

Claims 93-94 are further limiting wherein the chromosomal copy number is displayed in color on heat or line maps.

Ben-Dor et al., Koleszar et al., and Stanyon et al. make obvious an automated method for mapping genetic information, as discussed above.

Furthermore, Ben-Dor et al. teaches line maps. Koleszar et al. teaches the relevant user interface. Stanyon et al. teaches the color coded, binary (i.e. black/white) heat map.

Ben-Dor et al., Koleszar et al., and Stanyon et al. fail to teach division of the microarray of interest into an experimental and control matrix.

Figure 15 of Bodzin et al. illustrates the comparison of data between control and experiment data.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the radiation hybrid ordering method of Ben-Dor et al., the display method of Koleszar et al., and the heat maps of Stanyon et al. by use of the microarray division method of Bodzin et al. wherein the motivation would have been that the use of controls in microarrays provide a convenient means of normalization of the instant set of data [see paragraph 0037 of Bodzin et al.] It would have been further obvious to display chromosome copy numbers in color coding on the heat or line maps, because this display is an art accepted equivalent of the line and heat map shown in the combination of Ben-Dor et al. and Stanyon et al.

The following 35 U.S.C. 103 Rejections are newly applied:

35 U.S.C. 103 Rejection #6:

Claims 84 and 89 are rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Koleszar et al. in view of Stanyon et al. in view of Bodzin et al. as applied to claims 1-16, 18, 20-28, 29-33, 55-56, 81-83, 85-87, 90 and 93-94above, and further in view of McCully [issued 17 May 1983; filed 19 January 1982].

Claim 84 is further limiting comprising a "p value."

Claim 89 is further limiting comprising a relevance score limit value used as cutoff for values to display.

Ben-Dor et al., Koleszar et al., Stanyon et al., and Bodzin et al. make obvious an automated method for mapping genetic information, as discussed above.

Ben-Dor et al., Koleszar et al., Stanyon et al., and Bodzin et al. fail to use a p-value and a cutoff value.

The invention of McCully studies the therapeutic effects of salts as anti-neoplastic agents.

Specifically, example 7 in columns 8-9 of the invention uses a statistical technique to evaluate the effectiveness of the salts in malignancies in mice. Line 60-65 of column 8 of McCully state that the p values can be used to calculate differences between control and experimental samples in mice. This p value acts as a statistical cut off for determining deviation between a control and experimental sample.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the radiation hybrid ordering method of Ben-Dor et al., the display method of Koleszar et al., the heat maps of Stanyon et al. and the microarray division method of Bodzin et al. by use of the statistical criteria of McCully

because it is obvious to use a known technique to improve a similar method. In this instance, it the use the statistical criteria of McCully to analyze the microarrays in Bodzin et al. would have resulted in improved and more advanced statistical analysis. There would have been a reasonable expectation of success in combining these sources because the statistical techniques of McCully are generally applicable to the analysis of the other references.

The following 35 U.S.C. 103 Rejections are newly applied:

35 U.S.C. 103 Rejection #7:

Claim 92 is rejected under 35 U.S.C. 103(a) as being unpatentable over Ben-Dor et al. in view of Koleszar et al. in view of Stanyon et al. in view of Bodzin et al. as applied to claims 1-16, 18, 20-28, 29-33, 55-56, 81-83, 85-87, 90 and 93-94 above, and further in view of Anton [Elementary Linear Algebra, John Wiley and Sons: New York, 1987, pages 122-127].

Claim 92 is further limiting wherein the chromosomal copy number abnormality data is provided in columns interlaces with the columns of the expression data in the first and second matrices.

Ben-Dor et al., Koleszar et al., Stanyon et al., and Bodzin et al. make obvious an automated method for mapping genetic information, as discussed above.

Ben-Dor et al., Koleszar et al., Stanyon et al., and Bodzin et al. fail to teach the interlacing of columns in the matrices.

The textbook of Anton studies matrix manipulations for the purpose of solving linear algebra related problems.

Specifically, equation 3.15 of Anton on page 122 illustrates such a matrix manipulation in claim 92 by use of a cross product that "interlaces" members of separate vectors into a matrix.

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the radiation hybrid ordering method of Ben-Dor et al., the display method of Koleszar et al., the heat maps of Stanyon et al., and the microarray division method of Bodzin et al. by use of the cross products of Anton because it is obvious to provide a known technique to improve a known method. In this instance, it would have been obvious to use cross products to consolidate separate vector/matrix data into a single matrix for a more consolidates analysis of matrices relating to gene expression. There would have been a reasonable expectation of success in applying the linear algebra of Anton to the previous combination of studies because the linear algebraic techniques of Anton are generally applicable to most types of scientific analyses (including microarrays which are essentially linear algebraic matrices when represented mathematically).

Conclusion

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the

central PTO Fax Center. The faxing of such pages must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993)(See 37 CFR § 1.6(d)). The Central PTO Fax Center Number is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Negin, Ph.D., whose telephone number is (571) 272-1083. The examiner can normally be reached on Monday-Friday from 7am to 4pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's Supervisor, Marjorie Moran, Supervisory Patent Examiner, can be reached at (571) 272-0720.

Information regarding the status of the application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information on the PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

/RSN/
14 April 2008

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